

SEQUENCE LISTING

<110> FOSTER, Timothy
<120> METHODS FOR TREATING OR PREVENTING INFECTIONS FROM COAGULASE-NEGATIVE STAPHYLOCOCCI
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	130	135	140	

Thr Val Asn Glu Glu Ser Ile Ala Glu Thr Pro Lys Thr Ser Thr Thr
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Asp Ser Asn Asn Arg Glu Leu Gln Arg Val Thr Thr Asp Gln Ser Gly			
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His Tyr Gln Phe Asp Asn Leu Gln Asn Gly Thr Tyr Thr Val Glu Phe			
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Val Ala Lys Gly Thr Ile Asn Asn Ala Asp Asn Met Thr Val Asp Thr			
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Lys Lys Glu Glu Thr Asn Ser Asn Asp Ala Ile Glu Asn Arg Ser Lys
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Asp Ile Thr Gln Ser Thr Asn Val Asp Glu Asn Glu Ala Thr Phe
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Lys Glu Pro Ser Ser Val Glu Ser Ser Asn Ser Ser Met Asp Thr Ala
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Gln Gln Pro Ser His Thr Thr Ile Asn Ser Glu Ala Ser Ile Gln Thr
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Ser Asp Asn Glu Glu Asn Ser Arg Val Ser Asp Phe Ala Asn Ser Lys
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Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu Asp			
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Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu			
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Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys Ser			
625	630	635	640
Val Arg Thr Asp Glu Glu Gly Lys Tyr Gln Phe Asp Gly Leu Lys Asn			
645	650	655	
Gly Leu Thr Tyr Lys Ile Thr Phe Glu Thr Pro Glu Gly Tyr Thr Pro			
660	665	670	
Thr Leu Lys His Ser Gly Thr Asn Pro Ala Leu Asp Ser Glu Gly Asn			
675	680	685	
Ser Val Trp Val Thr Ile Asn Gly Gln Asp Asp Met Thr Ile Asp Ser			
690	695	700	
Gly Phe Tyr Gln Thr Pro Lys Tyr Ser Leu Gly Asn Tyr Val Trp Tyr			
705	710	715	720

Asp Thr Asn Lys Asp Gly Ile Gln Gly Asp Asp Glu Lys Gly Ile Ser
725 730 735

Gly Val Lys Val Thr Leu Lys Asp Glu Asn Gly Asn Ile Ile Ser Thr
740 745 750

Thr Thr Asp Glu Asn Gly Lys Tyr Gln Phe Asp Asn Leu Asn Ser
755 760 765

Gly Asn Tyr Ile Val His Phe Asp Lys Pro Ser Gly Met Thr Gln Thr
770 775 780

Thr Thr Asp Ser Gly Asp Asp Asp Glu Gln Asp Ala Asp Gly Glu Glu
785 790 795 800

Val His Val Thr Ile Thr Asp His Asp Asp Phe Ser Ile Asp Asn Gly
805 810 815

Tyr Tyr Asp Asp Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
820 825 830

Asp Asp Ser Asp
835 840 845

Ser Asp
850 855 860

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Gly Leu Asp
865 870 875 880

Asn Ser Ser Asp Lys Asn Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala
885 890 895

Asn Glu Asp His Asp Ser Lys Gly Thr Leu Leu Gly Ala Leu Phe Ala
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Gly Leu Gly Ala Leu Leu Leu Gly Lys Arg Arg Lys Asn Arg Lys Asn
915 920 925

Lys Asn
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<400> 12
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1 5

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Met Lys Lys Phe Asn Ile Lys His Ser Phe Met Leu Thr Gly Phe Ala
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ttc atg gta act aca tca tta ttc agt cac caa gca cat gct gaa ggt 96
Phe Met Val Thr Thr Ser Leu Phe Ser His Gln Ala His Ala Glu Gly
20 25 30

aat cat cct att gac att aat ttt tct aaa gat caa att gat aga aat 144
Asn His Pro Ile Asp Ile Asn Phe Ser Lys Asp Gln Ile Asp Arg Asn
35 40 45

aca gct aag agc aat att atc aat cga gtg aat gac act agt cgc aca 192
Thr Ala Lys Ser Asn Ile Ile Asn Arg Val Asn Asp Thr Ser Arg Thr
50 55 60

gga att agt atg aat tcg gat aat gat tta gat aca gat atc gtt tca 240
Gly Ile Ser Met Asn Ser Asp Asn Asp Leu Asp Thr Asp Ile Val Ser
65 70 75 80

aat agt gac tca gaa aat gac aca tat tta gat agt gat tca gat tca 288
Asn Ser Asp Ser Glu Asn Asp Thr Tyr Leu Asp Ser Asp Ser Asp Ser
85 90 95

gac agt gac tca gat tca gat agt gac tca gat tca gat agt gac tca 336
Asp Ser Asp Ser
100 105 110

gat tca gat agt gac tca gat tca gac agt gat tca gac tca gat agt 384
Asp Ser Asp Ser
115 120 125

gac tca gat tca gac agt gat tca gac tca gat agt gat tca gat tca 432
Asp Ser Asp Ser

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130	135	140	
gac agt gat tca gat tca gac agt gac tca gac tca gac agt gat tca			480
Asp Ser			
145	150	155	160
gat tca gat agt gat tca gat tca gat agt gat tca gat tca gat agt			528
Asp Ser			
165	170	175	
gat tca gat tca gac agt gac tca gac tca gac agt gat tca gat tca			576
Asp Ser			
180	185	190	
gat agt gat tca gac tca gat agt gac tca gat tca gat agt gat tca			624
Asp Ser			
195	200	205	
gac tct ggt aca agt tca ggt aag ggt tca cat acc gga aaa aaa cct			672
Asp Ser Gly Thr Ser Ser Gly Lys Gly Ser His Thr Gly Lys Lys Pro			
210	215	220	
ggg aac cct aaa gga aat aca aat aga cct tct caa aga cat acg aat			720
Gly Asn Pro Lys Gly Asn Thr Asn Arg Pro Ser Gln Arg His Thr Asn			
225	230	235	240
caa ccc caa agg cct aaa tac aat caa aca aat caa aac aat ata aac			768
Gln Pro Gln Arg Pro Lys Tyr Asn Gln Thr Asn Gln Asn Asn Ile Asn			
245	250	255	
aat ata aac cat aat att aat cat aca cgt act agt gga gat ggt gcg			816
Asn Ile Asn His Asn Ile Asn His Thr Arg Thr Ser Gly Asp Gly Ala			
260	265	270	
cct ttt aaa cgt caa caa aat att att aat tct aat tca ggt cat aga			864
Pro Phe Lys Arg Gln Gln Asn Ile Ile Asn Ser Asn Ser Gly His Arg			
275	280	285	
aat caa aat aat ata aat caa ttt ata tgg aac aaa aat ggc ttt ttt			912
Asn Gln Asn Asn Ile Asn Gln Phe Ile Trp Asn Lys Asn Gly Phe Phe			
290	295	300	
aaa tct caa aat aat acc gaa cat aga atg aat agt agc gat aat acc			960
Lys Ser Gln Asn Asn Thr Glu His Arg Met Asn Ser Ser Asp Asn Thr			
305	310	315	320
aat tca tta att agc aga ttc aga caa tta gcc acg ggt gct tat aag			1008
Asn Ser Leu Ile Ser Arg Phe Arg Gln Leu Ala Thr Gly Ala Tyr Lys			
325	330	335	
tac aat ccg ttt ttg att aat caa gta aaa aat ttg aat caa tta gat			1056
Tyr Asn Pro Phe Leu Ile Asn Gln Val Lys Asn Leu Asn Gln Leu Asp			
340	345	350	
gga aag gtg aca gat agt gac att tat agc ttg ttt aga aag caa tca			1104
Gly Lys Val Thr Asp Ser Asp Ile Tyr Ser Leu Phe Arg Lys Gln Ser			
355	360	365	
ttt aga gga aat gaa tat tta aat tca tta caa aaa ggg aca agc tat			1152
Phe Arg Gly Asn Glu Tyr Leu Asn Ser Leu Gln Lys Gly Thr Ser Tyr			
370	375	380	

ttc aga ttt caa tat ttt aat cca ctt aat tct agt aaa tac tat gaa Phe Arg Phe Gln Tyr Phe Asn Pro Leu Asn Ser Ser Lys Tyr Tyr Glu 385 390 395 400	1200
aat tta gat gat cag gtt tta gct tta att aca gga gaa atc ggc tca Asn Leu Asp Asp Gln Val Leu Ala Leu Ile Thr Gly Glu Ile Gly Ser 405 410 415	1248
atg cca gaa ctt aaa aaa cct acg gat aaa gaa gat aaa aat cat agc Met Pro Glu Leu Lys Lys Pro Thr Asp Lys Glu Asp Lys Asn His Ser 420 425 430	1296
gcc ttc aaa aac cat agt gca gat gag ata aca aca aat aat gat gga Ala Phe Lys Asn His Ser Ala Asp Glu Ile Thr Thr Asn Asn Asp Gly 435 440 445	1344
cac tcc aaa gat tat gat aag aaa aag aaa ata cat cga agt ctt tta His Ser Lys Asp Tyr Asp Lys Lys Lys Ile His Arg Ser Leu Leu 450 455 460	1392
tcg tta agt att gca ata att gga att ttt cta gga gtc act gga cta Ser Leu Ser Ile Ala Ile Ile Gly Ile Phe Leu Gly Val Thr Gly Leu 465 470 475 480	1440
tat atc ttt aga aga aaa aag taa Tyr Ile Phe Arg Arg Lys Lys 485	1464
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Thr Ala Lys Ser Asn Ile Ile Asn Arg Val Asn Asp Thr Ser Arg Thr 50 55 60	
Gly Ile Ser Met Asn Ser Asp Asn Asp Leu Asp Thr Asp Ile Val Ser 65 70 75 80	
Asn Ser Asp Ser Glu Asn Asp Thr Tyr Leu Asp Ser Asp Ser Asp Ser 85 90 95	
Asp Ser Asp Ser 100 105 110	

Asp Ser
115 120 125

Asp Ser
130 135 140

Asp Ser
145 150 155 160

Asp Ser
165 170 175

Asp Ser
180 185 190

Asp Ser
195 200 205

Asp Ser Gly Thr Ser Ser Gly Lys Gly Ser His Thr Gly Lys Lys Pro
210 215 220

Gly Asn Pro Lys Gly Asn Thr Asn Arg Pro Ser Gln Arg His Thr Asn
225 230 235 240

Gln Pro Gln Arg Pro Lys Tyr Asn Gln Thr Asn Gln Asn Asn Ile Asn
245 250 255

Asn Ile Asn His Asn Ile Asn His Thr Arg Thr Ser Gly Asp Gly Ala
260 265 270

Pro Phe Lys Arg Gln Gln Asn Ile Ile Asn Ser Asn Ser Gly His Arg
275 280 285

Asn Gln Asn Asn Ile Asn Gln Phe Ile Trp Asn Lys Asn Gly Phe Phe
290 295 300

Lys Ser Gln Asn Asn Thr Glu His Arg Met Asn Ser Ser Asp Asn Thr
305 310 315 320

Asn Ser Leu Ile Ser Arg Phe Arg Gln Leu Ala Thr Gly Ala Tyr Lys
325 330 335

Tyr Asn Pro Phe Leu Ile Asn Gln Val Lys Asn Leu Asn Gln Leu Asp
340 345 350

: Gly Lys Val Thr Asp Ser Asp Ile Tyr Ser Leu Phe Arg Lys Gln Ser
355 360 365

Phe Arg Gly Asn Glu Tyr Leu Asn Ser Leu Gln Lys Gly Thr Ser Tyr
370 375 380

Phe Arg Phe Gln Tyr Phe Asn Pro Leu Asn Ser Ser Lys Tyr Tyr Glu
385 390 395 400

Asn Leu Asp Asp Gln Val Leu Ala Leu Ile Thr Gly Glu Ile Gly Ser
405 410 415

Met Pro Glu Leu Lys Lys Pro Thr Asp Lys Glu Asp Lys Asn His Ser
420 425 430

Ala Phe Lys Asn His Ser Ala Asp Glu Ile Thr Thr Asn Asn Asp Gly
435 440 445

His Ser Lys Asp Tyr Asp Lys Lys Lys Ile His Arg Ser Leu Leu
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18

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<400> 16

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<210> 17
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Ala Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp His Asp Ser
20 25 30

Lys Gly Thr Leu Leu Gly Thr Leu Phe Ala Gly Leu Gly Ala Leu Leu
35 40 45

Leu Gly Arg Arg Arg Lys Lys Asp Asn Lys Glu Lys
50 55 60

<210> 19
<211> 60
<212> PRT
<213> Staphylococcus epidermidis

<400> 19

Ser Asp Ser Asp Ser Asp Ser Gly Leu Asp Asn Ser Ser Asp Lys Asn
1 5 10 15

Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp His Asp Ser
20 25 30

Lys Gly Thr Leu Leu Gly Ala Leu Phe Ala Gly Leu Gly Ala Leu Leu
35 40 45

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  50          55          60

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<212> PRT
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Thr Asn Asn Asp Gly His Ser Lys Asp Tyr Asp Lys Lys Lys Ile
20          25          30

His Arg Ser Leu Leu Ser Leu Ser Ile Ala Ile Ile Gly Ile Phe Leu
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Gly Val Thr Gly Leu Tyr Ile Phe Arg Arg Lys Lys
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<400> 23
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28

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<210> 29
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31

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33

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30

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<210> 38
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